

10/587,995

Sequence Alignment

ABP69565
 ID ABP69565 standard; protein; 704 AA.
 XX
 AC ABP69565;
 XX
 DT 15-JUN-2007 (revised)
 DT 20-JAN-2003 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 1612.
 XX
 KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
 KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
 KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
 KW antiarthritic; BOND_PC; axotrophin;
 KW membrane-associated RING-CH protein VII; axotrophin [Homo sapiens];
 KW MARCH7; AXO; MARCH-VII; DKF2P586F1122; AXOT; RNF177;
 KW membrane-associated ring finger (C3HC4) 7, isoform CRA_a;
 KW membrane-associated ring finger (C3HC4) 7, isoform CRA_a [Homo sapiens];
 KW unknown; unknown [Homo sapiens];
 KW membrane-associated ring finger (C3HC4) 7;
 KW Membrane-associated ring finger (C3HC4) 7 [Homo sapiens];
 KW unnamed protein product; unnamed protein product [Homo sapiens]; G05515;
 KW G06512; G08270; G016874; G046872; G04842; G06378.
 XX
 OS Homo sapiens.
 XX
 PN WO200270539-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 05-MAR-2002; 2002WO-US005095.
 XX
 PR 05-MAR-2001; 2001US-00799451.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Drmanac RT;
 XX
 DR WPI; 2002-759812/82.
 DR N-PSDB; ABZ11782.
 DR PC:NCBI; g12383066.
 DR PC:SWISSPROT; Q9H992.
 XX
 PT New polynucleotides comprising sequences assembled from expressed
 PT sequence tags (ESTs), useful for treating cell-proliferative,
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
 PT or coagulation disorders.

Qy	421	SHIFRRESNEVVHLEAQNDPLGAAANRPQASAASSATTGGSTSDSAQGGRRNTGISGILP	480
Db	421	SHIFRRESNEVVHLEAQNDPLGAAANRPQASAASSATTGGSTSDSAQGGRRNTGISGILP	480
Qy	481	GSLFRFAVPPALGSNLTDNVMITVDIIPSGWNSADGKSDKTSAPSRDPERLQKIKESLL	540
Db	481	GSLFRFAVPPALGSNLTDNVMITVDIIPSGWNSADGKSDKTSAPSRDPERLQKIKESLL	540
Qy	541	LEDSEEEGDLCRICQMAAASSSNLLIEPCKCTGSLQYVHQDCMKKWLQAKINSGSSLEA	600
Db	541	LEDSEEEGDLCRICQMAAASSSNLLIEPCKCTGSLQYVHQDCMKKWLQAKINSGSSLEA	600
Qy	601	VTTCELCKEKLNLNLEDFDIHELHRAHANEQAEYEFISSGLYLVLVLLHLCEQSFSDMMGN	660
Db	601	VTTCELCKEKLNLNLEDFDIHELHRAHANEQAEYEFISSGLYLVLVLLHLCEQSFSDMMGN	660
Qy	661	TNEPSTRVRFINLARTLQAHMEDLETSEDDSEEDGDHNRFTDIA	704
Db	661	TNEPSTRVRFINLARTLQAHMEDLETSEDDSEEDGDHNRFTDIA	704